

Db 241 PMSPALRLQRPPEPSAHAFCHR 265

RESULT 2

Q8SPF4

ID Q8SPF4 PRELIMINARY: PRT: 243 AA.

AC Q8SPF4.

DT 01-JUN-2002 (TREMblrel. 21, Created)

DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Inhibin alpha subunit (Fragment).

CN INHA.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

OX NCBI_TaxID:9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE:95251210; PubMed:7733505;

RA Hiendleder S., Janabber U., Weimann C., Grandke R.;

RT "RFLP markers for the porcine INHA locus.";

RL Anim. Genet. 26:131-132(1995).

RN [2]

RP SEQUENCE FROM N.A.

RA Hiendleder S., Reiner G., Seidermann H., Dzapo V.;

RT "Single nucleotide polymorphisms and PCR-RFLP linkage mapping of the

RT a-inhibin (INHA) gene, a qTL candidate for ovulation rate in swine.";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY028465; AAK37741.1; -

DR EMBL: AY028466; AAK37742.1; -

FT NON_TER

FT NON_TER

SQ SEQUENCE

243 AA: 26290 MW; 8F7E7E245BF7ED57 CRC64;

Query Match

Best Local Similarity 88.8%; Score 127; DB 6; Length 243;

Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PMSPALRLQRPPEPSAHAFCHR 25

Db 129 PMSPALRLQRPPEPSAHAFCHR 153

RESULT 3

Q98S00

ID Q98S00 PRELIMINARY: PRT: 329 AA.

AC Q98S00;

DT 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Inhibin-alpha.

OS Meleagris gallinapa (Common turkey).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.

OX NCBI_TaxID:9103;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Ovary;

RA Ahn J., You S., Kim H., Foster D.N., El Helawani M.E.;

RT "Molecular cloning of turkey inhibin-alpha and beta subunits.";

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF363377; AAK21264.1; -

DR HSP: P18075; BMP.

DR InterPro: IPR002405; Inhibin_alpha.

DR InterPro: IPR001839; TGFp.

DR Pfam: PF00019; TGF-beta; 1.

DR PRINTS: PR00669; INHIBINA.

DR ProDom: PD000357; TGFp; 1.

DR SMART: SM00204; TGFp; 1.

DR PROSITE: PS00250; TGF_BETA_1; 1.

KM Glycoprotein.

SQ SEQUENCE 329 AA: 35974 MW; E9G1AD113F5FC5C5 CRC64;

Query Match 65.7%; Score 94; DB 13; Length 329;

Best Local Similarity 68.0%; Pred. No. 3.2e-05;

Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PMSPALRLQRPPEPSAHAFCHR 25

Db 220 PMSPALRLQRPPEPSAHAFCHR 244

RESULT 4

Q9DAT0

ID Q9DAT0 PRELIMINARY: PRT: 116 AA.

AC Q9DAT0;

DT 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE 1600029114Rix protein.

GN 1600029114Rix.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID:10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6J; TISSUE-PLACENTA;

RX MEDLINE:21085660; PubMed:11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.;

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.;

RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.;

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.;

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.;

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.;

RA Schriml L.M., Straubli F., Suzuki K., Tomita M., Wagner L., Mashino T.;

RA Sekai K., Okido T., Furuno M., Aono H., Baldarelli K., Barish G.;

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.;

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.;

RA Gustincich S., Hill D., Holman M., Hume D.A., Kamiya M., Lee N.H.;

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.;

RA Nordone P., Ring B., Rineald M., Rodriguez I., Sakamoto N.;

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.;

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.;

RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.;

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL: AK005560; BAB24120.1; -

DR MGI:1917047; 1600029114Rix.

SQ SEQUENCE 116 AA: 14123 MW; 4629C27654E8C20D CRC64;

Query Match

Best Local Similarity 41.6%; Score 59.5; DB 11; Length 116;

Matches 13; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 SPAALRLQRPPEPSAHAFCHR 25

Db 91 SSAGIK-VTRPEPSAHAFCHR 112

RESULT 5

Q9DED3

ID Q9DED3 PRELIMINARY: PRT: 352 AA.

AC Q9DED3;

DT 01-MAR-2001 (TREMblrel. 16, Created)

DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Inhibin.

CN INH.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protactinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Tada T., Bado M., Hirono I., Takashima F., Aoki T.;
RT "Differential expression and cellular localization of activin and
inhibin mRNA in the rainbow trout ovary and testis";
RU Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC - - SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AB044566; BAB19272.1; -;
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGF.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00669; INHIBIN.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ SEQUENCE 352 AA; 39711 MW; ED9CCE860F912ED CRC64;

Query Match 41.38; Score 59; DB 13; Length 352;
Best Local Similarity 36.0%; Pred. No. 2.3;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 1 PMSPALRLQRPPEPSAHAFCH 25
DB 243 PWPSSIDLMPSSQKPEYSDCR 267

RESULT 6

ID O931X8 PRELIMINARY; PRT; 907 AA.
AC O931X8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein SC01292.
GN SC01292 OR SCBA036F5.03.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA Saunders D., Harris D.;
RU Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
KC Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RU Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE:97000351; PubMed-8843436;
RA Rodenhach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RU Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
KC Cerdeno A.M., Parkhill J., Barrell B.G., Challis G.L.,
RA Benley S.D., Chater K.F., Cerdeno-Tarraga A.M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces

RP coelicolor A3(2)";
RU Nature 417:141-147(2002).
DR EMBL: AL592292; CAC42839.1; -;
DR InterPro: IPR001232; SKP1.
KW Hypothetical protein.
SQ SEQUENCE 907 AA; 96786 MW; D149FDB39C7B53D0 CRC64;

Query Match 39.98; Score 57; DB 16; Length 907;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 4 PAALRLQRPPEPSAHAF 23
DB 676 PAALRLQRPVPSDSEWYC 695

RESULT 7

ID O8WYGB PRELIMINARY; PRT; 135 AA.
AC O8WYGB;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 15.1 kDa protein.
GN P25933.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.-W., Zhou X.M., Jiang H.-Q., Zhang P.-P.,
RA Qin W.-X., Huang Y., Qiu X.K., Qian L.F., He L.-P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
growth.";
RU Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF193049; AAG2477.1; -;
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 15056 MW; E85C66351D5F6B69 CRC64;

Query Match 39.58; Score 56.5; DB 4; Length 135;
Best Local Similarity 47.18; Pred. No. 2;
Matches 16; Conservative 3; Mismatches 4; Indels 11; Gaps 3;

OY 1 PMSPALRLQRPPEPSAHAFCH 25
DB 6 PMAEA--RLUGPAPAPATGCPNTAIAQSHR 37

RESULT 8

ID O9LBC9 PRELIMINARY; PRT; 1632 AA.
AC O9LBC9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Polyketide synthase.
GN EP08.
OS Polyangium cellulosum.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Sorangineae; Polyangiaceae; Polyangium.
OX NCBI_TaxID=56;
RN [1]
RP SEQUENCE FROM N.A.
KC STRAIN=SO CE90;
RX MEDLINE=20130945; PubMed-10662695;
RA Molnar I., Schnupp T., Ono M., Zirkle R.E., Milanow M.,
RA Novak-Thompson B., Engel N., Toupet C., Strattan A., Cyr D.D.,
RA Gorlach J., Mayo J.M., Hu A., Goff S., Schmidt J., Lison J.M.;
RT "The biosynthetic gene cluster for the microtubule-stabilizing agents
epothilones A and B from Sorangium cellulosum So ce90.";
RU Chem. Biol. 7:97-109(2000).

DR EMBL: AF210843; AAF62920.1; -
 DR InterPro: IPR001227; Ac_transferase.
 DR InterPro: IPR000794; Ketoacyl-synt.
 DR InterPro: IPR003880; Pantone_attach.
 DR Pfam: PF00698; Acyl_transf_1.
 DR Pfam: PF00109; ketoacyl-synt_1.
 DR Pfam: PF02801; ketoacyl-synt_C_1.
 DR Pfam: PF00550; pp-binding_1.
 DR PROSITE: PS50075; ACP_DOMAIN; 1.
 DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
 KW Phosphopantetheine; transferase.
 SQ SEQUENCE 1832 AA; 193106 MW; B0DBA54B2B57DC91 CRC64;

Query Match 38.8%; Score 55.5; DB 2; Length 1832;
 Best Local Similarity 48.1%; Pred. No. 34;
 Matches 13; Conservative 2; Mismatches 5; Indels 7; Gaps 2;

QY 1 PWSP---AALRLQRPPEPSNAFCH 24
 ||| :||||| :||
 DB 1123 FWPVEVGSRLTLQ---PSCGLMCH 1145

RESULT 9
 ID Q9K1Z8 PRELIMINARY; PRT; 1832 AA.
 AC Q9K1Z8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE EpOC.
 GN EpOC.
 OS Polyangium cellulosum.
 OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
 OC Myxococcales; Sorangineae; Polyangiaceae; Polyangium.
 OX NCBI_TaxId=56;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SM44;
 RX MEDLINE=20293058; PubMed=10831849;
 RA Julien B., Shah S., Ziermann R., Goldman R., Katz L., Khosla C.;
 RT "Isolation and characterization of the epothione biosynthetic gene
 cluster from Sorangium cellulosum.";
 RT Gene 249:153-160(2000).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SM44;
 RX MEDLINE=20115953; PubMed=10649995;
 RA Tang L., Shah S., Chung L., Carney J., Katz L., Khosla C., Julien B.;
 RT "Cloning and heterologous expression of the epothione gene cluster";
 RT Science 287:640-642(2000).
 RL EMBL: AF217189; AAF62882.1; -
 DR InterPro: IPR001227; Ac_transferase.
 DR InterPro: IPR000794; Ketoacyl-synt.
 DR InterPro: IPR003880; Pantone_attach.
 DR Pfam: PF00698; Acyl_transf_1.
 DR Pfam: PF00109; ketoacyl-synt_1.
 DR Pfam: PF02801; ketoacyl-synt_C_1.
 DR Pfam: PF00550; pp-binding_1.
 DR PROSITE: PS50075; ACP_DOMAIN; 1.
 DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
 KW Phosphopantetheine; transferase.
 SQ SEQUENCE 1832 AA; 193145 MW; C1EEDB8FA473C2D2 CRC64;

Query Match 38.8%; Score 55.5; DB 2; Length 1832;
 Best Local Similarity 48.1%; Pred. No. 34;
 Matches 13; Conservative 2; Mismatches 5; Indels 7; Gaps 2;

QY 1 PWSP---AALRLQRPPEPSNAFCH 24
 ||| :||||| :||
 DB 1123 FWPVEVGSRLTLQ---PSCGLMCH 1145

RESULT 10
 ID Q9B176 PRELIMINARY; PRT; 320 AA.
 AC Q9B176;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 33.9 kDa protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 GN NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-UTERUS;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC004304; AA004304.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 320 AA; 33851 MW; 64A68E268AB80EB CRC64;

Query Match 37.8%; Score 54; DB 4; Length 320;
 Best Local Similarity 41.7%; Pred. No. 10;
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 PWSPALRLQRPPEPSNAFCH 24
 ||| :||||| :||
 DB 53 PWAPAPRLGEAPGPRIVSYAH 76

RESULT 11
 ID Q8TAM0 PRELIMINARY; PRT; 368 AA.
 AC Q8TAM0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE G protein-coupled receptor 62.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC026357; AA026357.1; -
 KW Receptor.
 SQ SEQUENCE 368 AA; 37618 MW; 905D6A909812PBA CRC64;

Query Match 36.7%; Score 52.5; DB 4; Length 368;
 Best Local Similarity 61.1%; Pred. No. 19;
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 WSP-AALRLQRPPEPS 18
 ||| :||||| :||
 DB 321 WHPRALQLQRPPECPA 338

RESULT 12
 ID Q9JUM7 PRELIMINARY; PRT; 316 AA.
 AC Q9JUM7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Regulatory protein (3-COMPARTMENT signal transduction system,
 DE component PRR transmembrane protein).
 DE PRR OR RSP0850 OR RS01621.
 GN PRR OR RSP0850 OR RS01621.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; delta subdivision; Ralstonia group;

